

AMENDMENT

Please amend the above-captioned application as follows:

In the Specification:

Please amend the specification as follows:

Please replace the paragraph of lines 27 to 31, page 21, with the following amended paragraph:

B1
--Figures 8A and 8B ~~Figure 8~~. Fold of 3fxn obtained using 20 tertiary restraints compared with the native structure. This picture has been prepared using MOLMOL42. The native secondary structure boundaries (helices and β strands) have been superimposed on the predicted structure. A slight distortion of one helix (bottom right of the figure) and some distortions of the central β -sheet are noticeable.--

Please replace the paragraph of lines 1 to 2, page 22, with the following amended paragraph:

-- Figures 9A and 9B ~~Figure 9~~. Representative structure of 4fab obtained using 16 tertiary restraints compared with the native structure.--

In The Claims:

Please cancel claims 1 to 8, without prejudice.

B2
1 to 8. (Canceled, without prejudice)

9 to 13. (withdrawn)

14. (currently amended) A computer-assisted method for determining a three-dimensional structure of a target amino acid sequence using a computer comprising a processor configured to receive and output data in accordance with executable code, the method comprising:

(a) generating input data for the computer comprising: